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## We claim:

- Novel gene variants having of SEQ ID Nos. 1 and 2 of Signal Transdicer and Activator of Transcription-6 (STAT-6) Gene useful in pradicting susceptibility of a subject to atopic disorders, said gene variants having following characteristics:
  - (a) The SEQ ID No.1 has 1-392 contiguous nucleotides containing one or more group of GT dinucleotide polymorphisms at positions from \$25 to 168 of R1 locus, and.
  - (b) the SEQ ID No.2 has 1 to 336 contiguous nucleotides containing one or more group of GT dinucleotide polymorphisms at positions from \$7 to 116 bases of R3 lbcus.
- Novel gene variants as claimed in claim 1, wherein SEQ ID No.1 is associated with R1 locus and SEQ ID No.2 is associated with R3 locus of STAT-6 gene.
- 3. Noted yene variants as claimed in claim I, wherein a subject is lumant
- 4. Novel gene variants as claimed in claim 1, wherein atopic disorders are selected are from group comprising of asthma, atopic dermatitis, autoimmune disorders, inflammatory disorders, fibrosis or other known disorders of STAT-6.
- 5. Novel gene variants as claimed in claim 4, wherein atopic disorder is usitima.
- 6 Novel gene variants as claimed in claim 1, wherein said variants are useful are predicting and detecting limitans susceptible to atopic disorders selected from group comprising of assima, atopic dermatrits, autominime disorders, inflammatory disorders, fibrosis or other known disorders of STAT-6.
  - Novel gene variants as claimed in claim 6, wherem said variants are useful are predicting and detecting humans susceptible to asilima
- 8 Novel gene variants as claimed in claim 1, wherein said variants are pharmacogenetic markers for predicting and detecting humans susceptible to attoric disorders selected from group comprising of asthma, atopic disorders, autoimmune disorders, inflammatory disorders, filtrosis or other known disorders of STAT-6.

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- 9. Novel gene variants as claimed in claim 8, wherein said variants are pharmacogenetic markers for predicting and detecting humans susceptibles to asthmat.
- 10 Novel gene variants as claimed in claims 1 and 2, wherein said gene variants of locus R1\_R3 are associated with specific hapletypes 17, 15 and 16, 15
- II. Novel gene variants as claimed in claim:10, wherein the percentage frequency of RI\_R3 locus dinucleotide on haplotypes:17\_15 and 16\_15 is about 8.% and 20%, respectively in the patients.
- 12. Novel gene variants as claimed in claim 11, wherein the percentage frequency of R1 R3 locus dinucleotide on allele 17\_15 and 16\_15 is about 7.1% and 18.7% respectively in the patients.
- on 17 allele of R1 locus and on 15 allele of R3 locus of the STAT+ 6 gences having a 'p' value loss than 0.0031 and are associated with astlimit.
- 14 Novel gene variants as claimed in claim 1, wherein CA medicatide repeat is on 16 allele of R1 locus and on 15 allele of R3 locus of the STA1-6 gene having a p value less than 0.001 and are associated with assimp.
- 15. Novel gene variants as claimed in claim 1, wherein haplotypes 17 14 (CA repeat 17 in R1 locus and 14 in R3 locus of the STAT- 6 gene having a p' value less than 0.00001), 23\_16 (CA repeat 23 in R1 locus and 16 in R3 locus of the STAT- 6 gene having a p' value less than 0.00001) and 24\_16 (CA repeat 24 in R1 locus and 16 in R3 locus of the STAT- 6 gene baving a p' value less than 0.00001) are associated with protection from asthma.
  - 16 Novel gene variants as claumed in claim 1, wherein the percentage frequency of RI locus dinucleotide on allele 16 is about 32 % in the patients.
  - 17. Novel gene variants as claimed in claim 16, wherein the percentage frequency of Ril locus dinucleolide on allele is about 30.67 % in the patients.
  - 18. Novel gene variants as claimed in claim II, wherein the percentage frequency of IR3 locus dinucleotide on allele 15 is about 35 % in the patients.
  - 19. Novel gene variants as claimed in plain; 18, wherein the percentage frequency of R3 locus dinucleonde on allele 15 is about 32 % in the patients.

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- 20. A method of detecting gene variants having SEQ ID Nos. Using 2 of STAT 6 for detecting and predicting susceptibility of a subject to atopic disorders said method comprising the steps of:
  - (a) isolating DNA or RNA from samples selected from group comprising of whole blood, senten, saliva, tears, trine, fecal material, swear, buccal, skin or hair,
  - (b) designing and synthesizing primers having SEQ ID Nos. 3, 4, 5, 6 and
  - (c) amplifying the genomic DNA or RNA using printers having SEQ ID Nos. 3, 4, 5, 6 and 7;
  - (d) isolating and identifying SEQ ID No.1 using printer combinations: having SEQ ID Nos. 3, 4, and 7 and SEQ ID No. 2 using primer combinations having SEQ ID Nos. 5, 6 and 7,
  - (e) sequencing the isolated and identified SEQ ID Nos. 1 and 2 of step.
    (d), and
  - (f) validating and identifying the specific gene variants having SEO ID. Nos. 1 and 2 computationally by comparing with sum of START-6 gene, wherein the SEO ID Nos. 1 and 2 has following characteristics.
    - (i) the SEQ ID No. has 1-392 contiguous nucleoudes containing one or more group of GI diriudectide polymorphisms at positions from 125 to 168 bases of RI locus.
    - (ii) The SEQ ID No. has 1 to 336 contiguous nucleotides containing one or more group of UT dinudleotide polymorphisms at positions from 87 to 116 bases of R2 locus.
- 21 A method as claimed in claim 20, wherein SEQ ID No.1 is associated with R1 locus and SEQ ID No.2 is associated with R3 locus of STAT-6 gene.
- 22. A method as claimed in claim 20, wherein the subject is a human,
  - 23. A method as claimed in claim 20, wherein atopic disorders are scleeted from group comprising of asthme, atopic dermatitis, sufcommone disorders, inflammatory disorders, fibrosis or other known disorders of STAT-6 gene

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- 24. A method as claimed in claim 23, wherein atopic disortler selected is asthma.
- 25 A method as claimed in claim 20, wherein said variants are useful are predicting and detecting humans susceptible to atopic disorders selected from group comprising of asthma, atopic demantitis, autommune disorders, inflammatory disorders, fibrosis or other known disorders of STAT 6 gene.
- 26. A method as claimed in claim 25, wherein said variants are useful are predicting and detecting humans susceptible to asthma.
- 27. A method as claimed in claim 20, wherein said variants are phantiatogenetic markers for predicting and dejecting humans susceptible to atopic disorders selected from group comprising of asthma, atopic dermatitis, autoimmine disorders, inflammatory disorders, fibrosis or other known disorders of STAT-6 gene.
- 28. A, method as claimed in claim 27, wherein said variants are pharmacogenetic markers for predicting and detecting humans susceptible to astura.
- 29 Novel gone variants as claimed in claims 20 and 21 wherein said gene variants of locus R1 R3 are associated with specific hapterypes 17 15 and 16 15
  - 30. A method as claimed in claims 29, wherein the percentage frequency of R1\_R3 locus dinucleotide on allele 17\_15 and 16\_15 is about 8 % and 30%. respectively in the patients.
  - 31. At method as claimed in claim 30, wherein the percentage frequency of R1 R3 locus dimucleoude on haplotypes 17, 15 and 16, 15 is about 7.1 % and 18.7%, respectively in the patients.
  - 32. A method as claimed in claims 20, wherein CA midieotide repeat is on; I'll allele of R1 locus and on 15 allele of R3 locus of the STAT- 6 gene having a be value less than 0.0031 and are associated with asthma.
  - 33. A method as claimed in claim 20, wherein CA nucleotide repeat is on 16 affele of R1 locus and on 15 affele of R3 locus of the STAT, 6 gent having a pl value less than 0.001 and are associated with asthing.
  - 34. A method as claimed in claim 20, wherein haplotypes 17 14 (CA repeat 17 in R1 locus and 14 in R3 locus of the STAT-6 gene having a 'p' value less than 0.00001), 23 16 (CA repeat 23 in R1 locus and 16 in R3 locus of the STAT-6 gene having a 'p' value less than 0.00001) and 24 15 (CA repeat 24 in R1

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- locus and 16 in R3 locus of the STAT- 6 gene having a 'p' value less than 0.00001) are associated with protection from asthma.
- 35 A method as claimed in claim 20, wherein the percentage frequency of R., locus dinucleotide on allele 16 is about 32 % in the patients.
- 36. A method as claimed in claim; 35, wherein the percentage frequency of R1 locus dinucleotide on allele is about 30.67 % in the patients.
- 37 A method as claimed in claim 20, wherein the percentage frequency of R3 locus thrucleotide on allele 16 is about 35 % in the patients.
- 18. A method as claimed in claim 37, wherein the percentage frequency of R3 locus dinucleotide on allele 15 is about 32 % in the patients.
- 39. A method of detecting and predicting predisposition to atopic disorders by screening R1 and R3 locus of STAT-6 gene variants in a subject, said method comprising the steps of
  - (a) isolating DNA or RNA from samples selected from group complising of whole blood, semen, saliva, tears, urine, feeal material sivestibuccal, skin or hair,
  - (b) designing and synthesizing primers having SEQ ID Nos. 3, 4, 3, 6 and
  - (c) amplifying the genomic DNA or RNA using SEO ID Nos. 3. 4. 5. 6 and 7 by PCR;
  - (d) isolating and identifying SEQ ID No.1 justing printer combinations, having SEQ ID Nos. 3, 4, and 7 and SEQ ID No. 2 using primer combinations having SEQ ID Nos. 5, 6 and 7,
  - (e) sequencing the isolated and identified SEQ 1D Nos 1 and 2 of step
    (d), and
  - (f) sequencing the amplified PCR product of step (c), and
  - (g) validating and identifying the specific STAT-6 gene variants having SEQ ID Nos. 1 and 2 computationally by comparing with known START-6 gene, wherein the SEQ ID Nos. 1 and 2 has following characteristics
  - (i) the SEQ ID No has 1-392 configures intolegities containing one or more group of GT disurleptide polymorphisms at positions from 125 to 168 bases of locus RT and

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40 A method as claimed in claim 39, wherein SEQ ID No.1 is associated with R1 locus and SEQ ID No.2 is associated with R3 locus of STA1-6 gene.

positions from 87 to 116 bases of locus R3.

- 41. A method as claimed in claim 39, wherein the subject is a human.
- 42. A method as claimed in claim 41, wherein the atopic diseases are selected from group comprising of asthma, atopic dermalitis, autoulunune disorders, inflammatory disorders, florosis or other known disorders of STAT-6 gene.
- 43. A method as iclaimed in claim 42, wherein the latopic idisease selected in asthma.
- 44 A method as claimed in claim 39, wherein said variants are useful are predicting and detecting humans susceptible to atopic disorders selected from group comprising of asthma, atopic dermatitis, autoimmune disorders inflammatory disorders, fibrosis of other known disorders of STAT-6 general
- 45. A method as claimed in claim 44, wherein said variants are useful five predicting and detecting humans susceptible to asthma.
- 46. A method as claimed in claim 39, wherein said variants are plantification markers for predicting and detecting humans susceptible to atopic disorders selected from group comprising of asthma, atopic dermatitis, automitianted disorders, inflammatory disorders, fibrosis or other known disorders of STAT-6 general
- 47 A method as claimed in claim 46, wherein said variants are phinouscoperatic markers for predicting and detecting humans susceptible to asthma.
- 48. A method as claumed in claims 39 and 40, wherein said gene variants of locus.

  R1. R3 are associated with specific haplotypes 17, 15 and 16, 15
- 49. A method as claimed in claim 48, wherein the percentage frequency of R1\_R3 loons dimicleotide on haplotypes 17\_15 and 16\_15 is about 8 % and 20%, respectively in the patients.
- 50. At method, as claimed in claim: 49, wherein the percentage frequency of R1\_R3 locus dinucleotide on haplotypes 17\_15 and 16\_15 is about 7.2 % and 18.7%, respectively in the patients.

- 54. A method as claimed in claim 39, wherein CA nucleotide repeat is on 17 nlidle of R1 locus and on 15 allele of R1 locus of the STATe 6 gene having a p value less than 0.0031 and are associated with asthma.
- 52. A method as claimed in claim 39, wherein CA nucleotide repent is on 46 allele of R1 locus and on 15 allele of R3 locus of the STAT- 4 gene having a 'p' value less than 0.001 and are associated with asthina.
- S3. A method as claimed in claim 39, wherein haplotypes 3.7.14 (CA repeat 1.71n R1 locus and 14 in R3 locus of the STAT- 6 gene having a 'p' value less than 0.00001), 23\_16 (CA repeat 23 in R1 locus and 16 in R3 locus of the STAT- 6 gene having a 'p' value less than 0.00001) and 24\_16. (CA repeat 24 in R1 locus and 16 in R3 locus of the STAT- 6 gene having a 'p' value less than 0.00001) are associated with protection from asthma.
- 54. A method as claimed in claim 39, wherein the percentage frequency of R1 locus dinucleotide on allele 16 is about 32 % in the patients.
- 35. A method as claimed in claim 34, wherein the percentage frequency of R1 locas disucleotide on allele is about 30.67% in the patients.
  - 56: A method as claimed in claim 39, wherein the percentage frequency of R3 locus dinucleotide on allele 15 is about 35 % in the patients.
  - 57. A method as claimed in claim 56, wherein the percentage frequency of Rill locus dinucleotide on allele 15 is about 32 % in the patients.
  - 58 A method of preparing novel pharmacogenetic markers for detecting and predicting predisposition to atomic disorders of STAT-6 gene in a subject, said, method comprising steps of
    - (a) isolating DNA or RNA from samples selected from group comprising of whole blood, semen saliva, tears, urine; feeal material, sweat, huccal skin or hair,
    - (b) designing and synthesizing primers having SEQ ID Nos 3, 4, 5, 6 and
    - (c) amplifying the genomic DNA or RNA using printers having ShQ ID Nos. 3, 4, 5, 6 and 7.
    - (d) isolating and identifying SEQ ID No.1 using primer combinations having SEQ ID No. 3, 4, and 7 and SEQ ID No. 2 using primer combinations having SEQ ID Nos. 5, 6 and 7,

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- (e) sequencing the isolated and identified SEQ ID Nos. 1 and 2 of step
  (d), and
- (f) validating and identifying the specific gene variants having SEQ fb. Nos. 1 and 2 computationally by comparing with known START-6 gene, wherein the SEQ ID Nos. 1 and 2 has following characteristics:
  - (i) the SEQ ID No has 1-392 contiguous impleofides containing one or more group of GT dimudentials polymorphisms at positions from 125 to 168 bases, of locus R1 and
  - (ii) The SEQ ID No. has 1 to 336 contiguous mucleofides containing one or more group of GT dinucleofide polymorphisms at positions from 87 to 116 bases of locus R1.
- 15 59 A method gene variants as claimed in claim 58, wherein SEQ II) No.1 is associated with R1 locus and SEQ ID No.2 is associated with R3 locus at STAT-6 gene.
  - 60 A method as claimed in claim 58, wherein the subject is a human-
  - 61 A method as claimed in claim 58, wherein the atopic diseases are selected from group comprising of asthma, atopic dermattis, autoimmune disorders inflammatory disorders, fibrosis or other known disorders of STAU 6 gens.
  - 62 A method as claimed in claim 61, wherein the atopic discuse selected is asthma
  - 63 A method as claimed in claim 58, wherein said variants are useful are predicting and detecting humans susceptible to atopic disorders selected from group of asthma, atopic dermatitis, autoimmune disorders, inflammatory disorders, fibrosis or other known disorders of STAT-6 gene.
  - 64 A method as claimed in claim 63, wherein said variants are useful are predicting and detecting humans susceptible to asthma!
  - 65. A method as claimed in claim 58, wherein said variants are pharmacogenotic markers for predicting and detecting humans susceptible to storpe discribute selected from group comprising of asthma, atopic dermatitie, dutoimments

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- disorders, inflammatory disorders, fibrosis or other known disorders of STAT 6 gene.
- 66. A method as claimed in claim 65, wherem said variants are pharmacogenetic thankers for predicting and detecting humans susceptible to astimus.
- 67. A method as claimed in claims 58 and 59, wherein said gene variants of logus

  R1 R3 are associated with specific haplotypes 17 15 and 16 15
- cs. A method as claimed in claim 67, wherein the percentage frequency of R1\_R3 loous dinucleotide on haplotypes 17\_15 and 16\_15 is ellicit 8 % and 20%, respectively in the patients.
- 10 69 A method as claimed in claim 68, wherein the percentage frequency of RI\_R3 locus dinucleotide on hapletypes 17\_15 and 16\_15 is about 7.1 % and 18.7%, respectively in the patients
  - 70. A method as claimed in claim 58, wherein CA nucleotide repeat is for 17. allele of R1 locus and on 15 allele of R3 locus of the STATE 6 generatives a provided less than 0.0031 and are associated with asthma:
  - 71. A method as claimed in claim 58, wherein GA nucleotide repeat is 90; 16
    Allele of R1 locus and on 15 allele of R3 locus of the STAT-6 gene having a
    'b' value less than 0.001 and are associated with asthma.
  - 72: A method as claimed in claim 58, whereig haplotypes 17: 14 (CA repeat 17 in R1 locus and 14 m R3 locus of the STAT-6 gene having a p value less than 0,00001), 23 16 (CA repeat 23 in R1 locus and 15 in R2 locus of the STAT-6 gene having a p value less than 0,00001) and 24 16. (CA repeat 24 in R1 locus and 16 in R3 locus of the STAT-6 gene having a p value less than 0,00001) are associated with protection from asthma.
  - 73 A method as claimed in claim 58, wherein the percentage frequency of R1.

    locus dinucleotide on allele 16 is about 32 % in the patients.
  - 74. A method as claumed in claim 73, wherein the percentage frequency of R1.

    locus dinucleotide on alighe is about 30.67% in the patients.
  - 75. A method as claimed in claim 58, wherein the percentage trequency of R3 locus dinucleotide on allele 15 is about 35 % in the patients.
  - 76 A method as claimed in claim 75, wherein the percentage frequency of R3 locus dinucleotide on allele 15 is about 32 % in the patients.

- 77. Pharmacogenetic markers having SEQ ID Nos. 1 and 2 for detecting and predicting predisposition to atopic disorders of STAT-6 gene in a subject said markers comprising of following characteristics:
  - (a) the SEQ ID No.1 has 1-392 contiguous nucleolides containing one or more group of GT dinucleotide polymorphisms at positions from 125 to 168 of RI locus, and
  - (b) The SEQ ID No.2 has 1 to 336 contiguous nucleotides containing care or more group of GT dinucleotide polymorphisms at positions from 87 to 116 bases of R3 locus.
- 10 78. Pliannacogenetic markers as claimed in claim 77, Wherein SEQ ID No.1 is associated with R1 locus and SEQ ID No.2 is associated with R3 locus of STAT-6 gene.
  - 79 Pharmacogenetic markers as claimed in claim 77, wherein a subject is human.
  - 80. Pharmacogenetic markers as claimed in claim 79; wherein atopic disorders are selected are from group comprising of asthma, atopic derivatilis; autoimmune disorders, inflammatory disorders, fibrosis or other known, disorders of STAT-6 gene.
  - 81. Pharmacogenetic markets as claimed in claim 80, wherein atopid disorder its asthma.
  - 82. Pharmacogenetic markers as claimed in claim 77, whorein said variants are useful are predicting and detecting humans susceptible to atopic disorders selected from group comprising of asthma, atopic detriatitis, automating of asthma, atopic detriatitis, automating of STAT-6 gene.
  - 83. Pharmacogenetic markers as claimed in claim 82, wherein said variants are:
    useful are predicting and detecting humans susceptible to authors:
    - 84 Pharmacogenetic markers as claimed in claim 77, wherein said varieties are pharmacogenetic markers for predicting and detecting humans susceptible to atopic disorders selected from group comprising of asthma, atopic dermarities, autoimmune disorders, inflammatory disorders, fibrosis or other known disorders of STAT-6 gene.

- 86. A diagnostic kit for detecting and predicting predisposition to atopic diserders

  by screening STAT-6 gene variants in a subject, said method comprising the

  steps of:
  - (a) isolating DNA or RNA from samples selected from group comprising of whole blood, semen, saliva, tears, urine, fecal material, sweat, buccal, skin or hair,
  - (b) designing and synthesizing primers having SEQ ID Now 3, 4, 5 and 6
  - (a) amplifying the genomic DNA or RNA using SEQ ID Nos. 3, 4, 5 and
    6.
  - (d) isolating and identifying SEQ ID No.1 using primer combinations having SEQ ID Nos. B. 4, and 7 and SEQ ID/No. 2 using primer combinations having SEQ ID/Nos. 5, 6 and 7.
  - (e) sequencing the isolated and identified SEQ ID Nos 1 and 2.0f step.

    (d), and
  - (i) sequencing the amplified PCR product of step (c);
  - (g) validating and identifying the specific STAT-6 gene variants having SEQ ID Nos. 1 and 2 computationally by comparing with known START-6 gene, wherein the SEO ID Nos. 1 and 2 has following characteristics:
    - (i) the SEQ ID No.1 has 1-392 contiguous madecondes containing one or more group of GT dinucleutide golymorphisms of positions from 125 to 168 bases, and
    - (ii) the SEQ ID No.2 has 1 to 335 consignous mucleotides containing one or more group of GT diffucleotide polymorphisms at positions from 87 to 116 bases.
- 87. A kit as claimed in claim 86, wherein SEQ ID No.1 is associated with R1 locus and SEQ ID No.2 is associated with R3 locus of STAT-6 gene.
- 88. A kit as claimed in claim 86, wherein the subject is a human-

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- 89 A kit as claimed in claim 86, wherein the atopic diseases are selected from group comprising of asthma, atopic dermatilis, autoimmune disorders, inflammatory disorders, fibrosis or other known disorders of STAT-5 general
- 90. A kit as claimed in claim 89, wherein the atopic disease selected is asthmatic
- 91. A kit as claimed in claim 86, wherein said variants are useful and predicting and detecting humans susceptible to atopic disorders selected from urding of asthms, atopic dermatitis, autoimmute disorders, inflammatory disorders, fibrosis or other known disorders of STAT-6 gene.
- 92 A kit as claimed in claim 91, wherein said variants are useful are predicting and detecting humans susceptible to asthma.
- 93. A kit as claimed in claim 86, wherein said variants are pharmacogenetic markers for predicting and detecting humans susceptible to aionte disorders selected from group comprising of asitma, atopic dermatitis, automitune disorders, inflammatory disorders, fibrosis or other known disorders of STAT-6 gene.
- 94. A kit as claimed in claim 93, wherein said variable are plus markers for predicting and detecting humans susceptible to asthmat.
- 95. A kit is claimed in claims 85 and 87, wherein said gene variants of betts: R1
  R3 are associated with specific haplotypes 17\_15 and 16-15
- 96 A kit as claimed in claim 95, wherein the percentage frequency of R1 R3 locus dimedentide on baptotypes 1.7 15 and 16 15 is about 8 % and 20%, respectively in the patients
- 96. A kit as claimed in claim 96, wherein the percentage frequency of RUR3 locus dinucleotide on haplotypes 17 15 and 16 15 is about 71 % and 15 7%, respectively in the patients.
- 98: A kit as claimed in claim 86, wherem CA nucleotide repeat is out i 7 alless of R1 locus and on 15 alless of R3 locus of the STAT 6 genc having a plantile less than 0.0031 and are associated with asthma.
- 99) A kit as claimed in claim 86, wherein CA nucleonide repeat is on 16 alicle of R1 locus and on 15 aliele of R3 locus of the STAT. 6 gene having a p villuc loss than 0.001 and are associated with authora.
- 100 A kit as claimed in claim 86, wherein rapiditypes 12 14 (CA repeat 17 in R1 locus and 14 in R3 locus of the STAT 6 gene having a p value less

than 0.00001), 23\_16 (CA repeat 23 in R1 locus and 16 in R3 locus of the STAT-6 gene having a 'p' value less than 0.00001) and Z4\_16 (CA repeat 24 in R1 locus and 16 in R3 locus of the STAT-6 gene having a 'p' value less than 0.00001) are associated with protection from asthma.

- 101. A kit as claimed in claim 86, wherein the percentage frequency of R1 locus dinucleotide on allele 16 is about 32 % in the patients.
  - 102 A kit as claimed in claim 101, wherein the percentage frequency of R1 locus dinucleotide on allele is about 30.67% in the patients.
  - 103. A kit as claimed in claim 86, wherein the perdenting frequency of R2 locus dinucleotide on allele 15 is about 35 % in the partents.
  - 104 A kit as claimed in claim 103, wherein the percentage frequency of R3 locus dinucleotide on allele 15 is about 32 % in the patients.